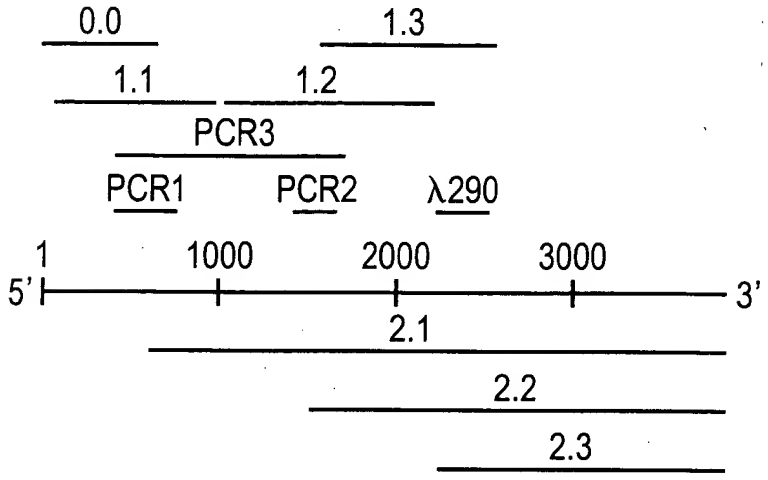

FIG. 1A

PCR Fragm./ CDNA clones	nt. positions
PCR1	388-731
PCR2	1575-1774
PCR3	388-1774
5'RACE	1-540
G6 library	1-641
1.1	53-1007
1.2	1018-2188
1.3	1553-2563
2.1	451-3837
2.2	1590-3983
2.3	2315-3983

FIG. 1B

```
GGCACGAGGCCGCGCCGAGGAGGCTGCCGCTCTGGCTTGCCAGTCCCCCGCCGCCGCTGCACACCGGACCCAGCCGCCGTGCCGCGGGCCATGGACCTGCCCAGGGGCCTGGTGGTGGCC  120
                                                                                                  M  D  L  P  R  G  L  V  V  A   10

TGGGCGCTCAGCCTGTGGCCAGGGTTCACGGACACCTTCAACATGGACACCAGGAAGCCCCGGGTCATCCCTGGCTCCAGGACCGCCTTCTTTGGCTACACAGTGCAGCAGCACGACATC  240
W  A  L  S  L  W  P  G  F  T  D  T  F  N  M  D  T  R  K  P  R  V  I  P  G  S  R  T  A  F  F  G  Y  T  V  Q  Q  H  D  I   50

AGTGGCAATAAGTGGCTGGTCGTGGGCGCCCCACTGGAAACCAATGGCTACCAGAAGACGGGAGACGTGTACAAGTGTCCAGTGATCCACGGGAACTGCACCAAACTCAACCTGGGAAGG  360
S  G  N  K  W  L  V  V  G  A  P  L  E  T  N  G  Y  Q  K  T  G  D  V  Y  K  C  P  V  I  H  G  N*  C  T  K  L  N  L  G  R   90

GTCACCCTGTCCAACGTGTCCGAGCGGAAAGACAACATGCGCCTCGGCCTTAGTCTCGCCACCAACCCCAAGGACAACAGCTTCCTGGCCTGCAGCCCCCTCTGGTCTCATGAGTGTGGG  480
V  T  L  S  N*  V  S  E  R  K  D  N  M  R  L  G  L  S  L  A  T  N  P  K  D  N  S  F  L  A  C  S  P  L  W  S  H  E  C  G  130

AGCTCCTACTACACCACAGGGATGTGTTCAAGAGTCAACTCCAACTTCAGGTTCTCCAAGACCGTGGCCCCAGCTCTCCAAAGGTGCCAGACCTACATGGACATCGTCATTGTCCTGGAT  600
S  S  Y  Y  T  T  G  M  C  S  R  V  N  S  N  F  R  F  S  K  T  V  A  P  A  L  Q  R  C  Q  T  Y  M  D  I  V  I  V  L  D  170

GGCTCCAACAGCATCTACCCCTGGGTGGAGGTTCAGCACTTCCTCATCAACATCCTGAAAAAGTTTTACATTGGCCCAGGGCAGATCCAGGTTGGAGTTGTGCAGTATGGCGAAGATGTG  720
G  S  N  S  I  Y  P  W  V  E  V  Q  H  F  L  I  N  I  L  K  K  F  Y  I  G  P  G  Q  I  Q  V  G  V  V  Q  Y  G  E  D  V  210

GTGCATGAGTTTCACCTCAACGACTACAGGTCTGTAAAAGATGTGGTGGAAGCTGCCAGCCACATTGAGCAGAGAGGAGGAACAGAGACCCGGACGGCATTTGGCATTGAATTTGCACGC  840
V  H  E  F  H  L  N  D  Y  R  S  V  K  D  V  V  E  A  A  S  H  I  E  Q  R  G  G  T  E  T  R  T  A  F  G  I  E  F  A  R  250
```

SEQ ID No. 1

FIG. 2A

SEQ ID No. 1

FIG. 2B

SEQ ID No. 1

FIG. 2C

```
AGGAAGCCTGCGCAGGACTGCTCCGCATACACGCTGTCCTTCGACACCACAGTCTTCATCATAGAGAGCACACGCCAGCGAGTGGCGGTGGAGGCCACACTGGAGAACAGGGGCGAGAAC 2640
R K P A Q D C S A Y T L S F D T T V F I I E S T R Q R V A V E A T L E N R G E N  850

GCCTACAGTACGGTCCTAAATATCTCGCAGTCAGCAAACCTGCAGTTTGCCAGCTTGATCCAGAAGGAGGACTCAGACGGTAGCATTGAGTGTGTGAACGAGGAGAGGAGGCTCCAGAAG 2760
A Y S T V L N* I S Q S A N L Q F A S L I Q K E D S D G S I E C V N E E R R L Q K  890

CAAGTCTGCAACGTCAGCTATCCCTTCTTCCGGGCCAAGGCCAAGGTGGCTTTCCGTCTTGATTCCGAGTTCAGCAAATCCATCTTCCTACACCACCTGGAGATCGAGCTCGCTGCAGGC 2880
Q V C N* V S Y P F F R A K A K V A F R L D S E F S K S I F L H H L E I E L A A G  930

AGTGACAGTAATGAGCGGGACAGCACCAAGGAAGACAACGTGGCCCCCTTACGCTTCCACCTCAAATACGAGGCTGACGTCCTCTTCACCAGGAGCAGCAGCCTGAGCCACTACGAGGTC 3000
S D S N E R D S T K E D N V A P L R F H L K Y E A D V L F T R S S S L S H Y E V  970

AAGCTCAACAGCTCGCTGGAGAGATACGATGGTATCGGGCCTCCCTTCAGCTGCATCTTCAGGATCCAGAACTTGGGCTTGTTCCCCATCCACGGGATGATGATGAAGATCACCATTCCC 3120
K L N* S S L E R Y D G I G P P F S C I F R I Q N L G L F P I H G M M M K I T I P  1010

ATCGCCACCAGGAGCGGCAACCGCCTACTGAAGCTGAGGGACTTCCTCACGGACGAGGCGAACACGTCCTGTAACATCTGGGGCAATAGCACTGAGTACCGGCCCACCCCAGTGGAGGAA 3240
I A T R S G N R L L K L R D F L T D E A N* T S C N I W G N* S T E Y R P T P V E E  1050

GACTTGCGTCGTGCTCCACAGCTGAATCACAGCAACTCTGATGTCGTCTCCATCAACTGCAATATACGGCTGGTCCCCAACCAGGAAATCAATTTCCATCTACTGGGGAACCTGTGGTTG 3360
D L R R A P Q L N* H S N S D V V S I N C N I R L V P N Q E I N F H L L G N L W L  1090
```

SEQ ID No. 1

FIG. 2D

AGGTCCCTAAAAGCACTCAAGTACAAATCCATGAAAATCATGGTCAACGCAGCCTTGCAGAGGCAGTTCCACAGCCCCTTCATCTTCCGTGAGGAGGATCCCAGCCGCCAGATCGAGTTT 3480
R S L K A L K Y K S M K I M V N A A L Q R Q F H S P F I F R E E D P S R Q I E F 1130

GAGATCTCCAAGCAAGAGGACTGGCAGGTCCCCATCTGGATCATTGTAGGCAGCACCCTGGGGGGCCTCCTACTGCTGGCCCTGCTGGTCCTGGCACTGCGGAAGCTCGGCTTCTTTAGA 3600
E I S K Q E D W Q V P I W I I V G S T L G G L L L L A L L V L A L R K L G F F R 1170

AGTGCCAGGCGCAGGAGGGAGCCTGGTCTGGACCCCACCCCCAAAGTGCTGGAGTGAGGCTCCAGAGGAGACTTTGAGTTGATGGGGGCCAGGACACCAGTCCAGGTAGTGTTGAGACCC 3720
S A R R R R E P G L D P T P K V L E 1188

AGGCCTGTGGCCCCACCGAGCTGGAGCGGAGAGGAAGCCAGCTGGCTTTGCACTTGACCTCATCTCCCGAGCAATGGCGCCTGCTCCCTCCAGAATGGAACTCAAGCTGGTTTTAAGTGG 3840

AACTGCCTACTGGGAGACTGGGACACCTTTACACAGACCCCTAGGGATTTAAAGGGACACCCCTACACACACCCAGGCCCACGCCAAGGCCTCCCTCAGGCTCTGTGGAGGGCATTTGCT 3960

GCCCCAGCTACTAAGGTGCTAGG 3983

SEQ ID No. 1

FIG. 2E

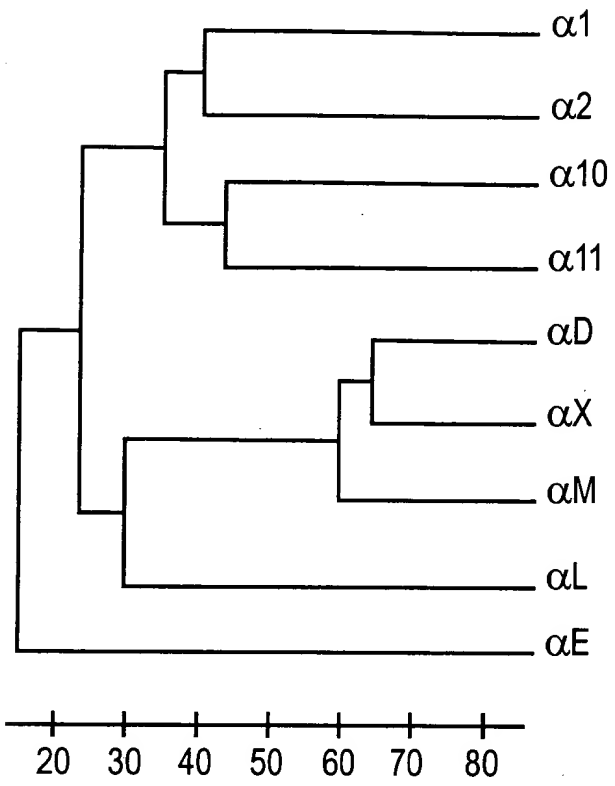

FIG. 3

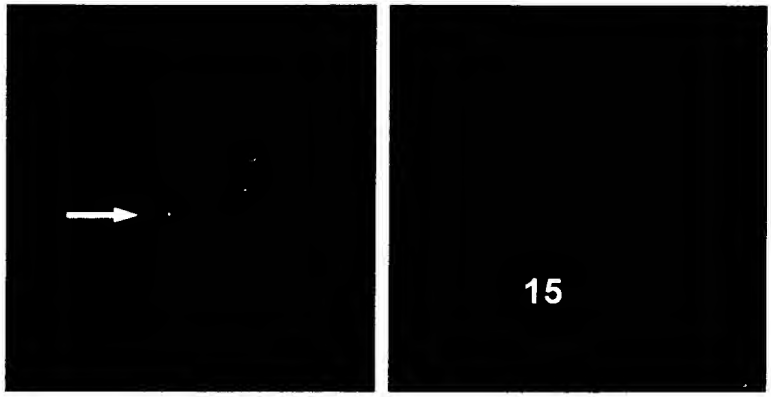
15

FIG. 4A

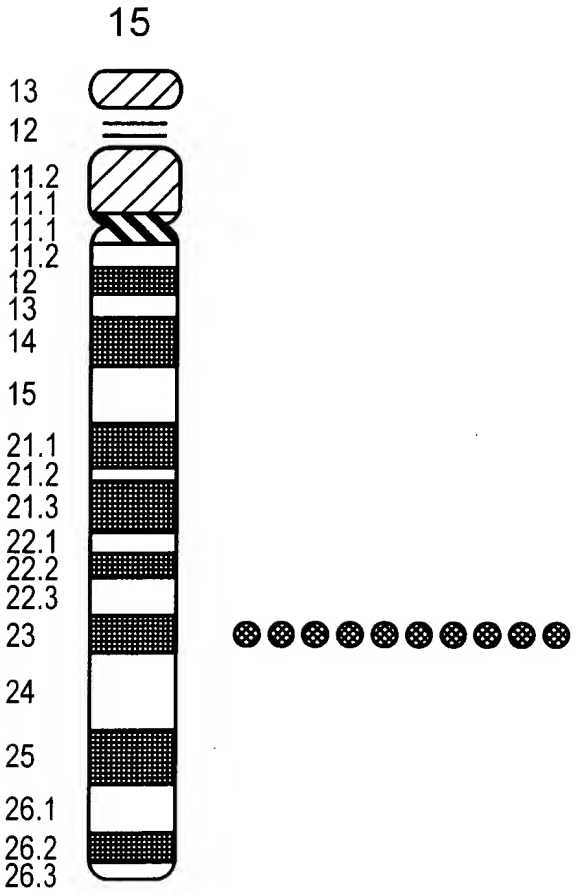
15
13
12
11.2
11.1
11.1
11.2
12
13
14
15
21.1
21.2
21.3
22.1
22.2
22.3
23
24
25
26.1
26.2
26.3

FIG. 4B

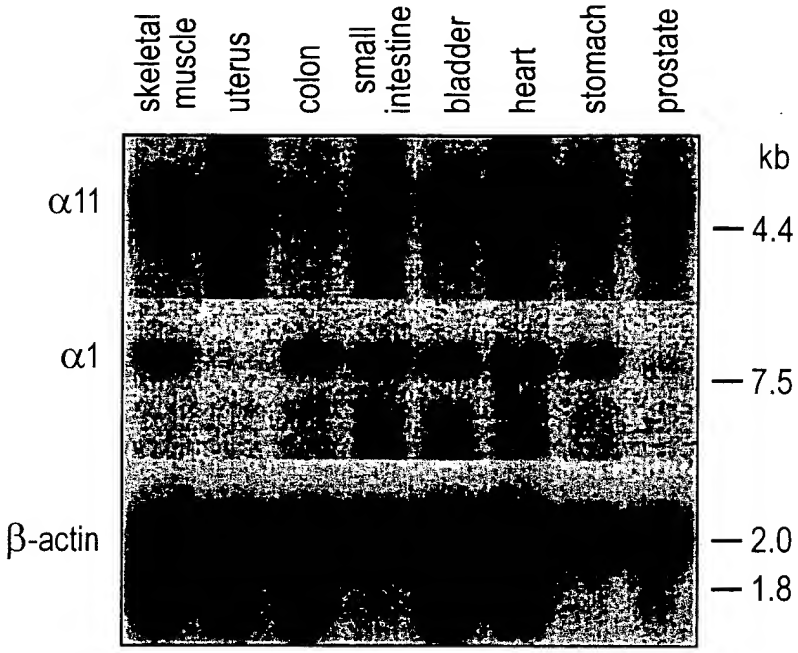
skeletal muscle
uterus
colon
small intestine
bladder
heart
stomach
prostate
kb
α11
α1
β-actin
4.4
7.5
2.0
1.8

FIG. 5

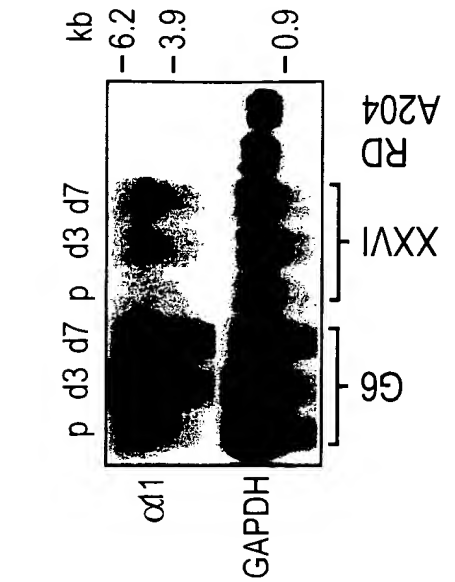

FIG. 6C

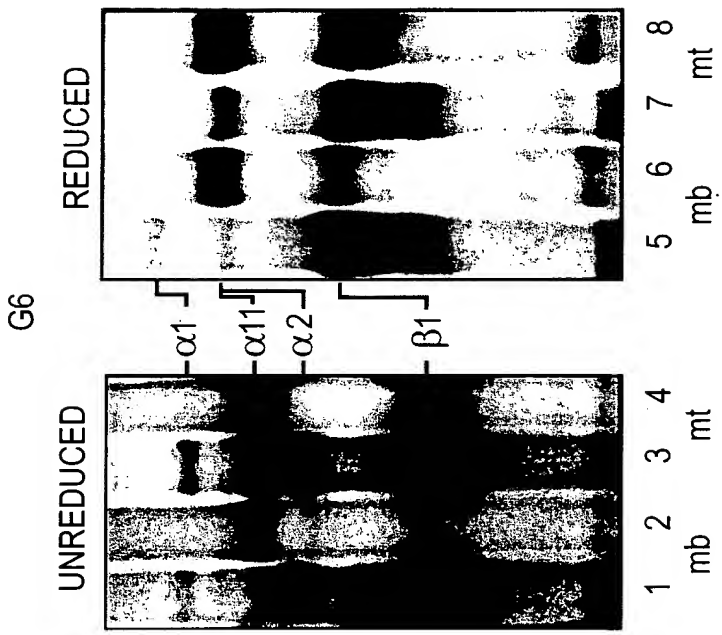

FIG. 6B

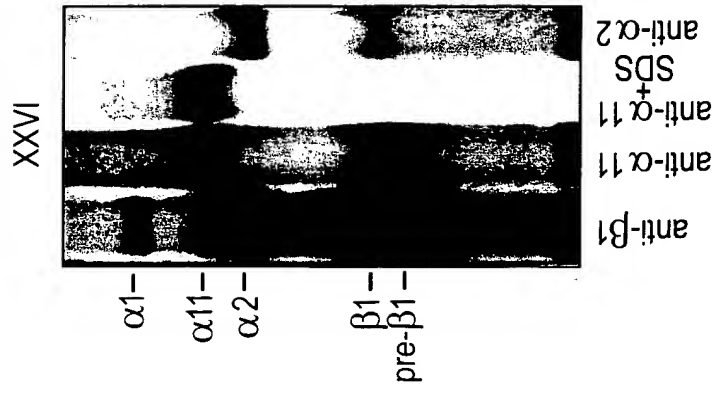

FIG. 6A

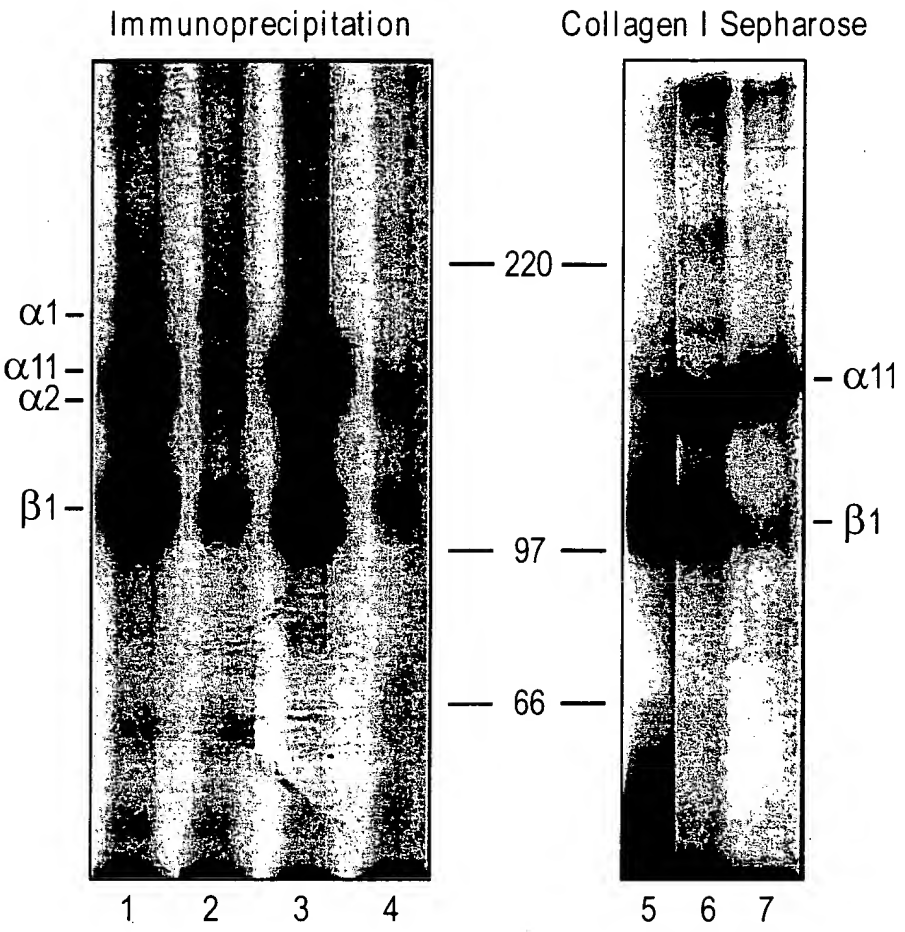
Immunoprecipitation
Collagen I Sepharose
α1
α11
α2
β1
220
97
66
α11
β1
1
2
3
4
5
6
7

FIG. 7A

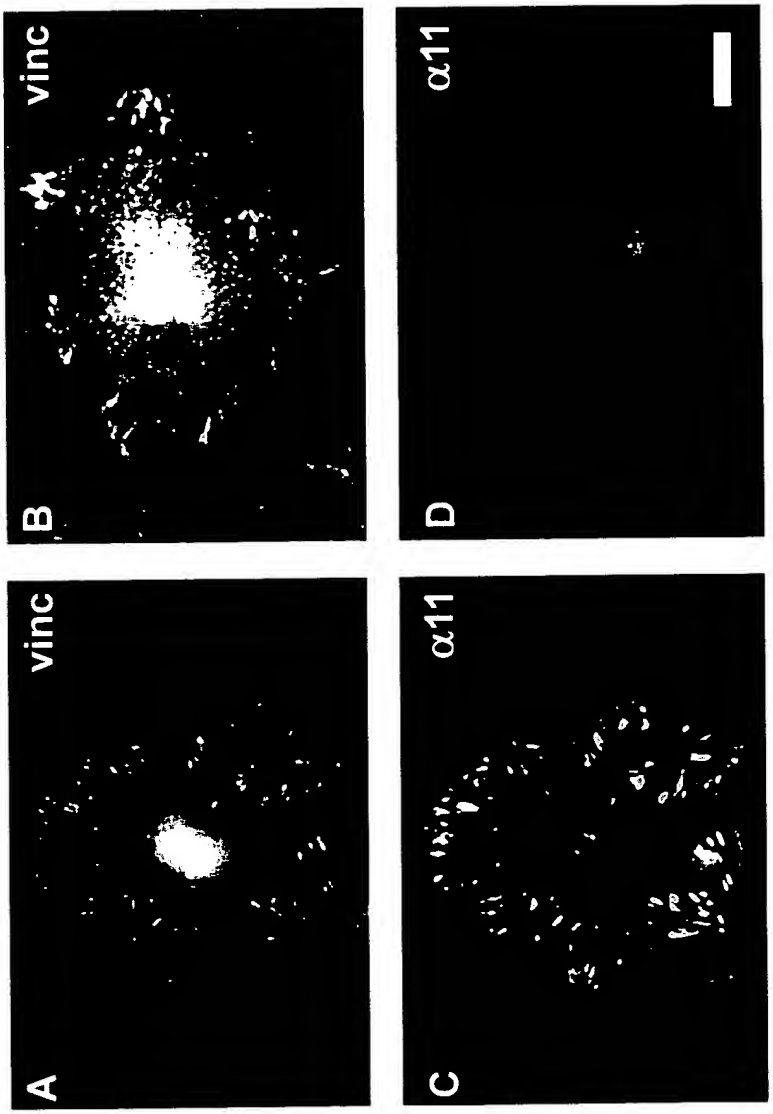

FIG. 7B

FIG. 8